SEQUENCE LISTING

<110> Cincinnati Children's Hospital Medical Center
      Robbins, Jeffrey

<120> A ROBUST, INDUCIBLE CARDIAC PREFERRED
   EXPRESSION SYSTEM FOR TRANSGENESIS

<130> CHM02 GN053

<150> 60/393,525
<151> 2002-07-03

<160> 10

<170> FastSEQ for Windows Version 4.0

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<223> Inducible Cardiac preferred promoter

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ctgtgcacac agagggtcga ggactggtgg tagagcctca agataaggat gatgctcaga 1740
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<210> 2
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<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence inserted in promoter.

<400> 2
tgcatgccct ga   12

<210> 3
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence excised from promoter.

<400> 3
tatctgccca tc   12

<210> 4
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence inserted into promoter with TetO binding
      sites.

<400> 4
tcgagtttac cactccctat cagtgataga gaaaagtgaa ag   42

<210> 5
<211> 627
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (21)...(602)
<223> ELC1-a

<400> 5
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                     Met Pro Pro Lys Lys Pro Glu Pro Lys Lys Glu
                       1               5                  10

act gcc aag ccg gct gca gcc cct gct cca gct gca tcc gca gct ccg    101
Thr Ala Lys Pro Ala Ala Ala Pro Ala Pro Ala Ala Ser Ala Ala Pro
              15                  20                  25

gag ccc ctc aag gac tct gcc ttt gac cca aag agt gtg aag ata gac    149
Glu Pro Leu Lys Asp Ser Ala Phe Asp Pro Lys Ser Val Lys Ile Asp
              30                  35                  40

ttc agt gct gac cag atc gaa gaa ttc aaa gag gcc ttt tca ttg ttt    197
Phe Ser Ala Asp Gln Ile Glu Glu Phe Lys Glu Ala Phe Ser Leu Phe
         45                  50                  55

gac cgg act cca acg gga gag atg aag atc acc tac ggg cag tgt ggg    245
Asp Arg Thr Pro Thr Gly Glu Met Lys Ile Thr Tyr Gly Gln Cys Gly
 60                  65                  70                  75

gac gtg ctg cgg gcc ctg ggc cag aac ccc acc aac gca gag gtg ctg    293
Asp Val Leu Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val Leu
              80                  85                  90

cgc gtt ttg ggc aaa ccc aag cct gaa gag atg agt tcc aag aca ctg    341
Arg Val Leu Gly Lys Pro Lys Pro Glu Glu Met Ser Ser Lys Thr Leu
              95                  100                 105

gac ttc gag atg ttc ctg ccc atc ctg caa cac atc tcc cgc aac aag    389
Asp Phe Glu Met Phe Leu Pro Ile Leu Gln His Ile Ser Arg Asn Lys
         110                 115                 120

gag cag ggc acc tat gag gac ttc gtg gag ggg ctg cgg gtc ttt gac    437
Glu Gln Gly Thr Tyr Glu Asp Phe Val Glu Gly Leu Arg Val Phe Asp
         125                 130                 135

aaa gaa agc aac ggc aca gtc atg ggt gcc gag ctt cgg cat gtc ctt    485
Lys Glu Ser Asn Gly Thr Val Met Gly Ala Glu Leu Arg His Val Leu
140                 145                 150                 155

gcc acc ctg gga gag aag atg agc gag gca gag gtg gag cag ctg ttg    533
Ala Thr Leu Gly Glu Lys Met Ser Glu Ala Glu Val Glu Gln Leu Leu
                 160                 165                 170

tct ggg cag gag gat gcc aat ggc tgc atc aac tat gaa gcc ttt gtc    581
Ser Gly Gln Glu Asp Ala Asn Gly Cys Ile Asn Tyr Glu Ala Phe Val
              175                 180                 185

aag cac atc atg tct ggg taa agcacgtttc tccagggtgg tcgac           627
Lys His Ile Met Ser Gly  *
         190
```

<210> 6
<211> 193
<212> PRT

<213> Mus musculus

<400> 6
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Ala Ala Pro Ala Pro Ala Ala Ser Ala Ala Pro Glu Pro Leu Lys Asp
            20                  25                  30
Ser Ala Phe Asp Pro Lys Ser Val Lys Ile Asp Phe Ser Ala Asp Gln
            35                  40                  45
Ile Glu Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Arg Thr Pro Thr
    50                  55                  60
Gly Glu Met Lys Ile Thr Tyr Gly Gln Cys Gly Asp Val Leu Arg Ala
65                  70                  75                  80
Leu Gly Gln Asn Pro Thr Asn Ala Glu Val Leu Arg Val Leu Gly Lys
                85                  90                  95
Pro Lys Pro Glu Glu Met Ser Ser Lys Thr Leu Asp Phe Glu Met Phe
                100                 105                 110
Leu Pro Ile Leu Gln His Ile Ser Arg Asn Lys Glu Gln Gly Thr Tyr
            115                 120                 125
Glu Asp Phe Val Glu Gly Leu Arg Val Phe Asp Lys Glu Ser Asn Gly
    130                 135                 140
Thr Val Met Gly Ala Glu Leu Arg His Val Leu Ala Thr Leu Gly Glu
145                 150                 155                 160
Lys Met Ser Glu Ala Glu Val Glu Gln Leu Leu Ser Gly Gln Glu Asp
                165                 170                 175
Ala Asn Gly Cys Ile Asn Tyr Glu Ala Phe Val Lys His Ile Met Ser
                180                 185                 190
Gly
```

<210> 7
<211> 1503
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (33)...(1295)
<223> GSK-CA

<400> 7
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                                     Met Ser Gly Arg Pro Arg Thr
                                     1               5

acc gcg ttt gcg gag agc tgc aag cca gtg cag cag cct tca gct ttt   101
Thr Ala Phe Ala Glu Ser Cys Lys Pro Val Gln Gln Pro Ser Ala Phe
            10                  15                  20

ggt agc atg aaa gtt agc aga gat aaa gat ggc agc aag gta acc aca   149
Gly Ser Met Lys Val Ser Arg Asp Lys Asp Gly Ser Lys Val Thr Thr
        25                  30                  35

gta gtg gca act cct ggc cag ggt cct gac agg cca cag gaa gtc agt   197
Val Val Ala Thr Pro Gly Gln Gly Pro Asp Arg Pro Gln Glu Val Ser
    40                  45                  50                  55
```

```
tat aca gac acg aaa gtg att gga aat gga tca ttt ggt gtg gta tat    245
Tyr Thr Asp Thr Lys Val Ile Gly Asn Gly Ser Phe Gly Val Val Tyr
            60                  65                  70

caa gcc aaa ctt tgt gat tct gga gaa ctg gtt gcc atc aag aaa gtt    293
Gln Ala Lys Leu Cys Asp Ser Gly Glu Leu Val Ala Ile Lys Lys Val
            75                  80                  85

cta cag gac aag cga ttt aag aac cga gag ctc cag atc atg aga aag    341
Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met Arg Lys
            90                  95                  100

cta gac cac tgt aac ata gtc cga ctg cgg tat ttc ttc tac tcg agt    389
Leu Asp His Cys Asn Ile Val Arg Leu Arg Tyr Phe Phe Tyr Ser Ser
            105                 110                 115

ggt gag aag aaa gat gag gtc tac ctt aac ctg gtg ctg gac tat gtt    437
Gly Glu Lys Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Asp Tyr Val
120                 125                 130                 135

ccg gag aca gtg tac aga gtc gcc aga cac tat agt cga gcc aag cag    485
Pro Glu Thr Val Tyr Arg Val Ala Arg His Tyr Ser Arg Ala Lys Gln
                140                 145                 150

aca ctc cct gtg atc tat gtc aag ttg tat atg tat cag ctg ttc aga    533
Thr Leu Pro Val Ile Tyr Val Lys Leu Tyr Met Tyr Gln Leu Phe Arg
                155                 160                 165

agt cta gcc tat atc cat tcc ttt gga atc tgc cat cga gac att aaa    581
Ser Leu Ala Tyr Ile His Ser Phe Gly Ile Cys His Arg Asp Ile Lys
            170                 175                 180

cca cag aac ctc ttg ttg gat cct gat aca gct gta tta aaa ctc tgt    629
Pro Gln Asn Leu Leu Leu Asp Pro Asp Thr Ala Val Leu Lys Leu Cys
            185                 190                 195

gac ttt gga agt gca aag cag ctg gtc cga gga gag ccc aat gtt tca    677
Asp Phe Gly Ser Ala Lys Gln Leu Val Arg Gly Glu Pro Asn Val Ser
200                 205                 210                 215

tat atc tgt tct cgg tac tac agg gca cca gag ttg atc ttt gga gcc    725
Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe Gly Ala
                220                 225                 230

act gat tac acg tcc agt ata gat gta tgg tct gca ggc tgt gtg ttg    773
Thr Asp Tyr Thr Ser Ser Ile Asp Val Trp Ser Ala Gly Cys Val Leu
            235                 240                 245

gct gaa ttg ttg cta gga caa cca ata ttt cct ggg gac agt ggt gtg    821
Ala Glu Leu Leu Leu Gly Gln Pro Ile Phe Pro Gly Asp Ser Gly Val
            250                 255                 260

gat cag ttg gtg gaa ata ata aag gtc cta gga aca cca aca agg gag    869
Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr Arg Glu
            265                 270                 275
```

```
caa att aga gaa atg aac cca aat tat aca gaa ttc aaa ttc cct caa    917
Gln Ile Arg Glu Met Asn Pro Asn Tyr Thr Glu Phe Lys Phe Pro Gln
280                 285             290                 295

atc aag gca cat cct tgg aca aag gtc ttc cgg ccc cga act cca cca    965
Ile Lys Ala His Pro Trp Thr Lys Val Phe Arg Pro Arg Thr Pro Pro
                300             305                 310

gag gca att gca ctg tgc agc cgt ctg ctg gag tac aca cct acc gcc    1013
Glu Ala Ile Ala Leu Cys Ser Arg Leu Leu Glu Tyr Thr Pro Thr Ala
            315                 320             325

cgg cta aca cca ctg gaa gct tgt gca cat tca ttt ttc gat gaa ttg    1061
Arg Leu Thr Pro Leu Glu Ala Cys Ala His Ser Phe Phe Asp Glu Leu
        330             335             340

cgg gac cca aat gtc aaa cta cca aat ggg cga gac aca cct gca ctc    1109
Arg Asp Pro Asn Val Lys Leu Pro Asn Gly Arg Asp Thr Pro Ala Leu
        345             350             355

ttc aac ttt acc act caa gaa ctg tca agt aac ccc cct ctg gcc acc    1157
Phe Asn Phe Thr Thr Gln Glu Leu Ser Ser Asn Pro Pro Leu Ala Thr
360             365             370             375

atc ctt atc cct cca cat gct cgg att cag gcc gct gct tca ccg cct    1205
Ile Leu Ile Pro Pro His Ala Arg Ile Gln Ala Ala Ala Ser Pro Pro
                380             385             390

gcc aac gcc aca gca gcc tca gat act aat gct gga gac cgt gga cag    1253
Ala Asn Ala Thr Ala Ala Ser Asp Thr Asn Ala Gly Asp Arg Gly Gln
            395             400             405

acc aat aac gcc gct tct gca tca gct tcc aac tcc acc tga            1295
Thr Asn Asn Ala Ala Ser Ala Ser Ala Ser Asn Ser Thr *
        410             415             420


acagccccca ggagccagct gcgcgggaaa gaccagcact tacttgagtg ccactcagca   1355
acactggtca cgtttggaaa gaaaattaaa aagaggaaaa caaaaacaaa aacaaaaaaa   1415
ccctgttcat tttagtgttc aatttttttt attgttgttc ttatttaacc ttgtaaaata   1475
tctatataaa tacaaaaaaa aaaaaaaa                                       1503

<210> 8
<211> 420
<212> PRT
<213> Mus musculus

<400> 8
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Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
                20                25                  30
Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
            35                40                  45
Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
        50                55                  60
Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
65                  70                75                      80
```

```
Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
            85                  90              95
Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
            100             105             110
Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
        115             120             125
Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
    130             135             140
His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
145             150             155             160
Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
            165             170             175
Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp
            180             185             190
Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
        195             200             205
Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala
    210             215             220
Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
225             230             235             240
Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
            245             250             255
Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
            260             265             270
Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
            275             280             285
Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val
    290             295             300
Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu
305             310             315             320
Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala
            325             330             335
His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn
            340             345             350
Gly Arg Asp Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser
            355             360             365
Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile
    370             375             380
Gln Ala Ala Ala Ser Pro Pro Ala Asn Ala Thr Ala Ala Ser Asp Thr
385             390             395             400
Asn Ala Gly Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala
            405             410             415
Ser Asn Ser Thr
            420


<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer used to amplify GSK

<400> 9
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<210> 10
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer used to amplify GSK

<400> 10
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ag   62